REMARKS UNDER 37 CFR § 1.111

Formal Matters

Claims 1-56 and 80-100 are pending after entry of the amendments set forth herein.

Claims 57-79 have been canceled above, without prejudice to the possibility of filing one or more continuing applications directed to the subject matter recited therein.

Claims 1-56 were examined. Claims 1-33 and 55-56 were rejected. Claims 20 and 34-55 were objected to. Claims 34-55 were indicated to have allowable subject matter.

Applicants respectfully request reconsideration of the application in view of the amendments and remarks made herein.

No new matter has been added.

The Office Action

Objections to Specification

In the Official Action of April 18, 2007, the specification was objected to as including hyperlinks in paragraphs [0006], [0013] and [0080]. In response thereto, Applicants have amended paragraphs [0006], [0013] and [0080] above to delete the hyperlinks previously contained therein. Accordingly, the Examiner is respectfully requested to reconsider and withdraw the objection to the specification as being no longer appropriate.

Claims Objections

Claims 20 and 55 were objected to for informalities. With regard to claim 20, Applicants have deleted the marked up language "~~values assessed~~". Brackets have been used to indicate the deletion to avoid confusion. Claim 55 has been amended to change "claim1" to –claim 1--. In view of the above amendments, the Examiner is respectfully requested to reconsider and withdraw the objections to claims 20 and 55 as being no longer appropriate.

Claims Rejected Under 35 U.S.C. Section 102(b) (Ben-Dor et al.)

Claims 1-3, 7, 12-15 and 27-28 were rejected under 35 U.S.C. Section 102(b) as being anticipated by Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278). The Examiner asserted that Ben-Dor et al. imports gene data from the Whitehead institute as an external source, and uses identifier in Table 4 to match them. The Examiner asserted that Fig. 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map.

Applicants respectfully traverse. It is respectfully submitted that the method described by Ben-Dor et al. does not import arbitrary gene- or protein- related data having identifiers, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al. map, as lines are drawn between the two maps to show the differences in locations. To even more clearly exclude Fig. 6 of Ben-Dor et al., which, it is respectfully submitted does not anticipate claim 1 for at least the reasons provided above, claim 1 has been amended to recite that that arbitrary gene- or protein-related data that is imported has not already been mapped to a chromosome map. Support for

this amendment can be found in Figs. 2A-11 and the descriptions thereof.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-3, 7, 12-15 and 27-28 under 35 U.S.C. Section 102(b) as being anticipated by Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278), as being clearly inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Stanyon et al.)

Claims 1, 16, 18, 20-26, 29-33 and 55-56 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155). The Examiner admitted that Ben-Dor et al. does not show expression matrices, statistical significance, additional information to the chromosome map, annotations, scores or statistical analyses of the matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines difference in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data having identifiers, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then

placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al. map, as lines are drawn between the two maps to show the differences in locations. To even more clearly exclude Fig. 6 of Ben-Dor et al., which, it is respectfully submitted does not anticipate claim 1 for at least the reasons provided above, claim 1 has been amended to recite that that arbitrary gene- or protein-related data that is imported has not already been mapped to a chromosome map.

It is further respectfully submitted that Stanyon et al. also fails to teach or suggest importing arbitrary gene- or protein- related data having identifiers, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Stanyon et al. teaches methods of painting probes to mouse and rat chromosomes , imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content. Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claim 1. Further, the rat chromosomes are painted experimentally with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data, not by reading an identifier associated with the data, matching it to a predefined identifier on a chromosome map and then overlaying the data on the chromosome map.

Nor does Stanyon teach or suggest displaying an expression matrix adjacent a chromosome map.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1, 16, 18, 20-26, 29-33 and 55-56 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155), as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al.)

Claims 1 and 4-11 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al. (U.S. Patent No. 6,519,583). The Examiner admitted that Ben-Dor et al. does not disclose the use of a display to analyze the data (i.e. zooming in to display the additional data as claimed in the instant set of claims), but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of Koleszar et al. because Koleszar et al. has the advantage of displaying the genomic data of Ben-Dor et al. in a more convenient and user-friendly format.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data having identifiers, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al. map, as lines are drawn between the two maps to show the differences in locations. To even more clearly exclude Fig. 6 of Ben-Dor et al., which, it is respectfully submitted does not anticipate claim 1

for at least the reasons provided above, claim 1 has been amended to recite that that arbitrary gene- or protein-related data that is imported has not already been mapped to a chromosome map.

It is further respectfully submitted that Koleszar et al. also fails to teach or suggest importing arbitrary gene- or protein- related data having identifiers, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Koleszar et al. teaches methods of graphically displaying computer-based biomolecular sequence information, which may be composed of nucleotide or amino acid sequence information, or both. Thus, Koleszar et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Koleszar et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination would still not meet all of the recitations of claim 1, for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1 and 4-11 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al. (U.S. Patent No. 6,519,583), as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Singer et al.)

Claims 1 and 16-19 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Singer et al. (U.S. Patent No. 5,866,331). The Examiner admitted that Ben-Dor et al. does not disclose the use of heat maps on a plurality of matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of Singer et al. by the use of heat maps because Singer et al. uses advance mapping techniques to better detect hybridization to short sequences.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data having identifiers, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the

genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al. map, as lines are drawn between the two maps to show the differences in locations. To even more clearly exclude Fig. 6 of Ben-Dor et al., which, it is respectfully submitted does not anticipate claim 1 for at least the reasons provided above, claim 1 has been amended to recite that that arbitrary gene- or protein-related data that is imported has not already been mapped to a chromosome map.

It is further respectfully submitted that Singer et al. also fails to teach or suggest importing arbitrary gene- or protein- related data having identifiers, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Singer et al. merely teaches methods for accurately determining the total emission intensity of a single fluorochrome, under imaging conditions. Thus, Singer et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Singer et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination

would still not meet all of the recitations of claim 1, for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1 and 16-19 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Singer et al. (U.S. Patent No. 5,866,331), as being inappropriate.

Allowable Subject Matter

Claims 34-54 were objected to as being dependent upon a rejection base claim, but the Examiner indicated that these claims would be allowable if rewritten into independent form to include all of the limitations of the base claim and any intervening claims.

In response thereto, Applicants have submitted new claims 80-100 above. Claim 80 is an independent claims that incorporates the recitations of claim 1 (prior to the above amendment of claim 1) and claim 34. Claims 81-100 correspond to claims 35-54, respectively, but depend from claim 80.

Accordingly, the Examiner is respectfully requested to indicate the allowance of claims 80-100 in the next Official Action.

Conclusion

Applicants submit that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-1078, order number 10020503-2.

Respectfully submitted,

Date: 7/17/07

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